



## SEQUENCE LISTING

<110> Svendsen, Allan  
Kjaerulff, Soren  
Bisgard-Frantzen, Henrik  
Andersen, Carsten

<120> Alpha-amylase variants

<130> 5709.200-US

<160> 31

<170> PatentIn version 3.1

<210> 1

<211> 485

<212> PRT

<213> Bacillus sp.

<400> 1

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr  
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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala  
20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp  
35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly  
65 70 75 80

Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly  
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp  
100 105 110

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn  
115 120 125

Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp  
130 135 140

RECEIVED

MAY 28 2002

TECH CENTER 1600/2900

Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr  
145 150 155 160

His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys  
165 170 175

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp  
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met  
195 200 205

Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr  
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His  
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr  
245 250 255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu  
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val  
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly  
290 295 300

Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys  
305 310 315 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro  
325 330 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala  
340 345 350

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr  
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser  
 370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr  
 385 390 395 400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu  
 405 410 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp  
 420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly  
 435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile  
 450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser  
 465 470 475 480

Val Trp Val Lys Gln  
 485

<210> 2  
 <211> 485  
 <212> PRT  
 <213> Bacillus sp.

<400> 2

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His  
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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser  
 20 25 30

Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp  
 35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
 50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly  
 65 70 75 80

Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly  
85 90 95

Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp  
100 105 110

Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn  
115 120 125

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp  
130 135 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr  
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg  
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp  
180 185 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met  
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr  
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His  
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala  
245 250 255

Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu  
260 265 270

Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val  
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly  
290 295 300

Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys  
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro  
325 330 335

Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala  
340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr  
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala  
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr  
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu  
405 410 415

Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp  
420 425 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly  
435 440 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile  
450 455 460

Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser  
465 470 475 480

Ile Trp Val Lys Arg  
485

<210> 3  
<211> 514  
<212> PRT  
<213> Bacillus stearothermophilus

<400> 3

Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu

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Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn  
20 25 30

Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys  
35 40 45

Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp  
50 55 60

Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr  
65 70 75 80

Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met  
85 90 95

Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly  
100 105 110

Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln  
115 120 125

Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe  
130 135 140

Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His  
145 150 155 160

Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr  
165 170 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu  
180 185 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His  
195 200 205

Pro Glu Val Val Thr Glu Leu Lys Ser Trp Gly Lys Trp Tyr Val Asn  
210 215 220

Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys  
225 230 235 240

Phe Ser Phe Phe Pro Asp Trp Leu Ser Asp Val Arg Ser Gln Thr Gly  
245 250 255

Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys  
260 265 270

Leu His Asn Tyr Ile Met Lys Thr Asn Gly Thr Met Ser Leu Phe Asp  
275 280 285

Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Thr  
290 295 300

Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro  
305 310 315 320

Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln  
325 330 335

Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala  
340 345 350

Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp  
355 360 365

Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile  
370 375 380

Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His  
385 390 395 400

Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val  
405 410 415

Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro  
420 425 430

Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val  
435 440 445

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser  
450 455 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp  
465 470 475 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Trp Ser Ile Thr Thr  
485 490 495

Arg Pro Trp Thr Asp Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val  
500 505 510

Ala Trp

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<211> 483  
<212> PRT  
<213> Bacillus licheniformis

<400> 4

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro  
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Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu  
20 25 30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly  
35 40 45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu  
50 55 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys  
65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn  
85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr  
100 105 110

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val  
115 120 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro



130		135		140
Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe				
145		150		155 160
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys				
	165		170	175
Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn				
	180		185	190
Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val				
	195		200	205
Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln				
	210		215	220
Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe				
225		230		235 240
Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met				
	245		250	255
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn				
	260		265	270
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu				
	275		280	285
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met				
	290		295	300
Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser				
305		310		315 320
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu				
	325		330	335
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu				
	340		345	350
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly				
	355		360	365

C1  
Cont.

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile  
370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His  
385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp  
405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro  
420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr  
435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser  
450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr  
465 470 475 480

Val Gln Arg

<210> 5  
<211> 480  
<212> PRT  
<213> Bacillus amyloliquefaciens

<400> 5

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp  
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Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp  
20 25 30

Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser  
35 40 45

Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu  
50 55 60

Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu  
65 70 75 80

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr  
85 90 95

Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp  
100 105 110

Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser  
115 120 125

Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg  
130 135 140

Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly  
145 150 155 160

Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg  
165 170 175

Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn  
180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val  
195 200 205

Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser  
210 215 220

Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe  
225 230 235 240

Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met  
245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn  
260 265 270

Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu  
275 280 285

His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met

290                      295                      300  
 Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala  
 305                      310                      315                      320  
 Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu  
 325                      330                      335  
 Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu  
 340                      345                      350  
 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly  
 355                      360                      365  
 Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile  
 370                      375                      380  
 Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His  
 385                      390                      395                      400  
 Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp  
 405                      410                      415  
 Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro  
 420                      425                      430  
 Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr  
 435                      440                      445  
 Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser  
 450                      455                      460  
 Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr  
 465                      470                      475                      480  
 <210> 6  
 <211> 485  
 <212> PRT  
 <213> Bacillus sp.  
 <400> 6  
 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr  
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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Asn Ser Asp Ala Ser  
20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp  
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly  
65 70 75 80

Thr Arg Ser Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly  
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp  
100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn  
115 120 125

Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp  
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Ser Phe Lys Trp Arg Trp Tyr  
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Arg Leu Asn Asn Arg  
165 170 175

Ile Tyr Lys Phe Arg Gly His Gly Lys Ala Trp Asp Trp Glu Val Asp  
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met  
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr  
210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His  
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala  
245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu  
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Gln Lys Thr Asn Trp Asn His Ser Val  
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly  
290 295 300

Gly Asn Tyr Asp Met Arg Asn Ile Phe Asn Gly Thr Val Val Gln Arg  
305 310 315 320

His Pro Ser His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro  
325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala  
340 345 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr  
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser  
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys  
385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu  
405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp  
420 425 430

Gly Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly  
435 440 445

Gln Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile  
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser

465

470

475

480

Ile Trp Val Asn Lys  
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<210> 7  
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<212> PRT  
<213> Bacillus sp.

<400> 7

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr  
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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala  
20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp  
35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly  
65 70 75 80

Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly  
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp  
100 105 110

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn  
115 120 125

Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp  
130 135 140

Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr  
145 150 155 160

His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys  
165 170 175

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp  
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met  
195 200 205

Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr  
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His  
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr  
245 250 255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu  
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val  
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly  
290 295 300

Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys  
305 310 315 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro  
325 330 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala  
340 345 350

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr  
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser  
370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr  
385 390 395 400



Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu  
 405 410 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp  
 420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly  
 435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile  
 450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser  
 465 470 475 480

Val Trp Val Lys Gln  
 485

<210> 8  
 <211> 485  
 <212> PRT  
 <213> Bacillus sp.

<400> 8

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His  
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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser  
 20 25 30

Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp  
 35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
 50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly  
 65 70 75 80

Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly  
 85 90 95

Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp  
 100 105 110

Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn  
115 120 125

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp  
130 135 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr  
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg  
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp  
180 185 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met  
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr  
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His  
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala  
245 250 255

Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu  
260 265 270

Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val  
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly  
290 295 300

Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys  
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro  
325 330 335

Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala  
 340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr  
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala  
 370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr  
 385 390 395 400

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu  
 405 410 415

Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp  
 420 425 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly  
 435 440 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile  
 450 455 460

Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser  
 465 470 475 480

Ile Trp Val Lys Arg  
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<210> 9

<211> 1455

<212> DNA

<213> Bacillus sp.

<400> 9

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 gctgtatgga tcccacctgc atggaagggg acttcccaga atgatgtagg ttatggagcc 180  
 tatgatattat atgatcttgg agagtttaac cagaagggga cggttcgtac aaaatatgga 240  
 acacgcaacc agctacaggc tgcggtgacc tcttttaaaaa ataacggcat tcaggtatat 300

ggtgatgtcg tcatgaatca taaaggtgga gcagatggta cggaaattgt aaatgcggta	360
gaagtgaatc ggagcaaccg aaaccaggaa acctcaggag agtatgcaat agaagcgtgg	420
acaaagtttg attttcctgg aagaggaaat aaccattcca gctttaagtg gcgctggtat	480
cattttgatg ggacagattg ggatcagtca cgccagcttc aaaacaaaat atataaattc	540
aggggaacag gcaaggcctg ggactgggaa gtcgatacag agaatggcaa ctatgactat	600
cttatgtatg cagacgtgga tatggatcac ccagaagtaa tacatgaact tagaaactgg	660
ggagtgtggt atacgaatac actgaacctt gatggattta gaatagatgc agtgaaacat	720
ataaaatata gctttacgag agattggctt acacatgtgc gtaacaccac aggtaaacca	780
atgtttgcag tggctgagtt ttggaaaaat gaccttgggtg caattgaaaa ctatttgaat	840
aaaacaagtt ggaatcactc ggtgtttgat gttcctctcc actataattt gtacaatgca	900
tctaatagcg gtggttatta tgatatgaga aatattttaa atggttctgt ggtgcaaaaa	960
catccaacac atgccgttac ttttgttgat aaccatgatt ctcagcccgg ggaagcattg	1020
gaatcctttg ttcaacaatg gtttaaacca cttgcatatg cattggttct gacaagggaa	1080
caaggttatc cttccgtatt ttatggggat tactacggta tccaaccca tgggtgtccg	1140
gctatgaaat ctaaaataga ccctcttctg caggcacgtc aaacttttgc ctatggtacg	1200
cagcatgatt actttgatca tcatgatatt atcggttgga caagagaggg aaatagctcc	1260
catccaaatt caggccttgc caccattatg tcagatgggtc cagggtggtaa caaatggatg	1320
tatgtgggga aaaataaagc gggacaagtt tggagagata ttaccggaaa taggacaggc	1380
accgtcacia ttaatgcaga cggatggggt aatttctctg ttaatggagg gtccgtttcg	1440
gtttgggtga agcaa	1455

<210> 10  
 <211> 1455  
 <212> DNA  
 <213> Bacillus sp.

<400> 10	
catcataatg ggacaaatgg gacgatgatg caatactttg aatggcaott gctaataatgat	60
gggaatcact ggaatagatt aagagatgat gctagtaatc taagaaatag aggtataacc	120
gctattttggga ttccgcctgc ctggaaaggg acttcgcaaa atgatgtggg gtatggagcc	180
tatgatcttt atgatttagg ggaatttaat caaaagggga cggttcgtac taagtatggg	240
acacgtagtc aattggagtc tgccatccat gctttaaaga ataatggcgt tcaagtttat	300

gggatgtag tgatgaacca taaaggagga gctgatgcta cagaaaacgt tcttgctgtc	360
gaggtgaatc caaataaccg gaatcaagaa atatctgggg actacacaat tgaggcttgg	420
actaagtttg attttccagg gaggggtaat acatactcag actttaaatg gcgttggtat	480
catttcgatg gtgtagattg ggatcaatca cgacaattcc aaaatcgtat ctacaaattc	540
cgaggtgatg gtaaggcatg ggattgggaa gtagattcgg aaaatggaaa ttatgattat	600
ttaatgtatg cagatgtaga tatggatcat ccggaggtag taaatgagct tagaagatgg	660
ggagaatggt atacaaatac attaaatctt gatggattta ggatcgatgc ggtgaagcat	720
attaaatata gctttacacg tgattgggtg acccatgtaa gaaacgcaac gggaaaagaa	780
atgtttgctg ttgctgaatt ttggaaaaat gatttaggtg ccttggagaa ctatttaaat	840
aaaacaaact ggaatcattc tgtctttgat gtcccccttc attataatct ttataacgcg	900
tcaaatagtg gaggcaacta tgacatggca aaacttctta atggaacggt tgttcaaaag	960
catccaatgc atgccgtaac ttttgtggat aatcacgatt ctcaacctgg ggaatcatta	1020
gaatcatttg tacaagaatg gtttaagcca cttgcttatg cgcttatttt aacaagagaa	1080
caaggctatc cctctgtctt ctatgggtgac tactatggaa ttccaacaca tagtgtccca	1140
gcaatgaaag ccaagattga tccaatctta gaggcgcgtc aaaattttgc atatggaaca	1200
caacatgatt attttgacca tcataatata atcggatgga cacgtgaagg aaataccacg	1260
catccaatt caggacttgc gactatcatg tcggatgggc cagggggaga gaaatggatg	1320
tacgtagggc aaaataaagc aggtcaagtt tggcatgaca taactggaaa taaaccagga	1380
acagttacga tcaatgcaga tggatgggct aatttttcag taaatggagg atctgtttcc	1440
atttgggtga aacga	1455

<210> 11  
 <211> 1548  
 <212> DNA  
 <213> Bacillus stearothermophilus

<400> 11	
gccgcaccgt ttaacggcac catgatgcag tattttgaat ggtacttgcc ggatgatggc	60
acgttatgga ccaaagtggc caatgaagcc aacaacttat ccagccttgg catcaccgct	120
ctttggctgc cgcccgtta caaaggaaca agccgcagcg acgtagggta cggagtatac	180
gacttgatg acctcggcga attcaatcaa aaagggaccg tccgcacaaa atacggaaca	240
aaagctcaat atcttcaagc cattcaagcc gccacgccg ctggaatgca agtgtacgcc	300

gatgtcgtgt tcgaccataa aggcggcgct gacggcacgg aatgggtgga cgccgtcgaa 360  
gtcaatccgt ccgaccgcaa ccaagaaatc tcgggcacct atcaaatcca agcatggacg 420  
aaatttgatt ttcccgggcg gggcaacacc tactccagct ttaagtggcg ctggtaccat 480  
tttgacggcg ttgattggga cgaaagccga aaattgagcc gcatttaca attccgcggc 540  
atcggcaaag cgtgggattg ggaagtagac acggaaaacg gaaactatga ctacttaatg 600  
tatgccgacc ttgatatgga tcatcccgaa gtcgtgaccg agctgaaaaa ctgggggaaa 660  
tggtatgtca acacaacgaa cattgatggg ttccggcttg atgccgtcaa gcatattaag 720  
ttcagttttt ttctgattg gttgtcgtat gtgcgttctc agactggcaa gccgctattt 780  
accgtcgggg aatattggag ctatgacatc aacaagttgc acaattacat tacgaaaaca 840  
gacggaacga tgtctttgtt tgatgccccg ttacacaaca aattttatac cgcttccaaa 900  
tcagggggcg catttgatat gcgcacgtta atgaccaata ctctcatgaa agatcaaccg 960  
acattggccg tcaccttcgt tgataatcat gacaccgaac ccggccaagc gctgcagtca 1020  
tgggtcgacc catggttcaa accgttggct tacgccttta ttctaactcg gcaggaagga 1080  
taccgtgcg tcttttatgg tgactattat ggcatccac aatataacat tccttcgctg 1140  
aaaagcaaaa tcgatccgct cctcatcgcg cgcagggatt atgcttacgg aacgcaacat 1200  
gattatcttg atcactccga catcatcggg tggacaaggg aagggggcac tgaaaaacca 1260  
ggatccggac tggccgact gatcaccgat gggccgggag gaagcaaatg gatgtacgtt 1320  
ggcaaacaac acgctggaaa agtgttctat gaccttaccg gcaaccggag tgacaccgtc 1380  
accatcaaca gtgatggatg gggggaattc aaagtcaatg gcggttcggt ttcggtttgg 1440  
gttcctagaa aaacgaccgt ttctaccatc gtcggccga tcacaaccog accgtggact 1500  
ggtgaattcg tccgttgga cgaaccacgg ttggtggcat ggccttga 1548

<210> 12  
<211> 1920  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> misc\_feature  
<222> (421)..(1872)  
<223> CDS

<400> 12  
cggaagattg gaagtacaaa aataagcaaa agattgtcaa tcatgtcatg agccatgcgg 60

gagacggaaa aatcgtctta atgcacgata tttatgcaac gttcgcagat gctgctgaag	120
agattattaa aaagctgaaa gcaaaaggct atcaattggg aactgtatct cagcttgaag	180
aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgccatata ggcgcttttc	240
ttttggaaga aaatataggg aaaatgggtac ttgttaaaaa ttcggaatat ttatacaaca	300
tcatatgttt cacattgaaa ggggaggaga atcatgaaac aacaaaaacg gctttacgcc	360
cgattgctga cgctgttatt tgcgctcatc ttcttgctgc ctcatctctgc agcagcggcg	420
gcaaacttta atgggacgct gatgcagtat tttgaatggg acatgcccaa tgacggccaa	480
cattggaggc gtttgcaaaa cgactcggca tttttggctg aacacgggat tactgccgtc	540
tggattcccc cgcatataa gggaacgagc caagcggatg tgggctacgg tgcttacgac	600
ctttatgatt taggggagtt tcatcaaaaa gggacgggtc ggacaaagta cggcacaaaa	660
ggagagctgc aatctgcgat caaaagtctt cattcccgcg acattaacgt ttacggggat	720
gtggctcatca accacaaagg cggcgctgat gcgaccgaag atgtaaccgc ggttgaagtc	780
gatcccgctg accgcaaccg cgtaatttca ggagaacacc taattaaagc ctggacacat	840
tttcattttc cggggcgcgg cagcacatac agcgatttta aatggcattg gtaccatttt	900
gacggaaccg attgggacga gtcccgaag ctgaaccgca tctataagtt tcaaggaaaag	960
gcttgggatt ggggaagtttc caatgaaaac ggcaactatg attatttgat gtatgccgac	1020
atcgattatg accatcctga tgcgcagca gaaattaaga gatggggcac ttggtatgcc	1080
aatgaactgc aattggacgg tttccgtctt gatgctgtca aacacattaa attttctttt	1140
ttgcgggatt gggttaatca tgtcaggga aaaacgggga aggaaatgtt tacggtagct	1200
gaatattggc agaattgactt gggcgcgctg gaaaactatt tgaacaaaac aaattttaat	1260
cattcagtgt ttgacgtgcc gcttcattat cagttccatg ctgcatcgac acagggaggc	1320
ggctatgata tgaggaaatt gctgaacggt acggctggtt ccaagcatcc gttgaaatcg	1380
gttacatttg tcgataacca tgatacacag ccggggcaat cgcttgagtc gactgtccaa	1440
acatggttta agccgcttgc ttacgctttt attctcacia gggaatctgg atacctcag	1500
gttttctacg gggatatgta cgggacgaaa ggagactccc agcgcgaaat tcctgccttg	1560
aaacacaaaa ttgaaccgat cttaaaagcg agaaaacagt atgcgtacgg agcacagcat	1620
gattatttcg accaccatga cattgtcggc tggacaaggg aaggcgacag ctcggttgca	1680
aattcagggt tggcggcatt aataacagac ggaccgggtg gggcaaagcg aatgtatgtc	1740
ggccggcaaa acgccggtga gacatggcat gacattaccg gaaaccgttc ggagccgggt	1800

C1  
Cmt

gtcatcaatt cggaaggctg gggagagttt cacgtaaacy gcgggtcggt ttcaatttat	1860
gttcaaagat agaagagcag agaggacgga tttcctgaag gaaatccggt tttttat	1920

<210> 13  
 <211> 1455  
 <212> DNA  
 <213> Bacillus sp.

<400> 13	
catcataatg gaacaaatgg tactatgatg caatatttcg aatggatattt gccaaatgac	60
gggaatcatt ggaacaggtt gagggatgac gcagctaact taaagagtaa agggataaca	120
gctgtatgga tcccacctgc atggaagggg acttcccaga atgatgtagg ttatggagcc	180
tatgatttat atgatcttg agagttaa acagaagggga cggttcgtac aaaatatgga	240
acacgcaacc agctacaggc tgcggtgacc tctttaaaaa ataacggcat tcaggatatat	300
ggtgatgtcg tcatgaatca taaaggtgga gcagatggta cggaaattgt aaatgcggta	360
gaagtgaatc ggagcaaccg aaaccaggaa acctcaggag agtatgcaat agaagcgtgg	420
acaaagtttg attttcctgg aagaggaaat aaccattcca gctttaagtgc gcgctgggat	480
cattttgatg ggacagattg ggatcagtca cgccagcttc aaaacaaaat atataaattc	540
aggggaacag gcaaggcctg ggactgggaa gtcgatacag agaatggcaa ctatgactat	600
cttatgtatg cagacgtgga tatggatcac ccagaagtaa tacatgaact tagaaactgg	660
ggagtgtggt atacgaatac actgaacctt gatggattta gaatagatgc agtgaaacat	720
ataaaatata gctttacgag agattggctt acacatgtgc gtaacaccac aggtaaacca	780
atgtttgcag tggctgagtt ttggaaaaat gaccttggtg caattgaaaa ctatttgaat	840
aaaacaagtt ggaatcactc ggtgtttgat gttcctctcc actataattt gtacaatgca	900
tctaatagcg gtggttatta tgatatgaga aatattttta atggttctgt ggtgcaaaaa	960
catccaacac atgccgttac ttttggtgat aaccatgatt ctgagcccgg ggaagcattg	1020
gaatcctttg ttcaacaatg gtttaaacca cttgcatatg cattggttct gacaagggaa	1080
caagggtatc cttccgtatt ttatggggat tactacggta tccaaccca tgggtgttccg	1140
gctatgaaat ctaaaataga ccctcttctg caggcacgtc aaacttttgc ctatggtacg	1200
cagcatgatt actttgatca tcatgatatt atcggttgga caagagaggg aaatagctcc	1260
catccaaatt caggccttgc caccattatg tcagatggtc cagggtggtaa caaatggatg	1320
tatgtgggga aaaataaagc gggacaagtt tggagagata ttaccggaaa taggacaggc	1380

C1  
 CNT



accgtcaciaa ttaatgcaga cggatggggg aatttctctg ttaatggagg gtccgtttcg 1440  
gtttgggtga agcaa 1455

<210> 14  
<211> 1455  
<212> DNA  
<213> Bacillus sp.

<400> 14  
catcataatg ggacaaatgg gacgatgatg caatactttg aatggcactt gcctaataatg 60  
gggaatcact ggaatagatt aagagatgat gctagtaatc taagaaatag aggtataacc 120  
gctattttgga ttccgcctgc ctggaaaggg acttcgcaaa atgatgtggg gtatggagcc 180  
tatgatcttt atgatttagg ggaatttaaat caaaagggga cggttcgtac taagtatggg 240  
acacgtagtc aattggagtc tgccatccat gctttaaaga ataatggcgt tcaagtttat 300  
ggggatgtag tgatgaacca taaaggagga gctgatgcta cagaaaacgt tcttgctgtc 360  
gaggtgaatc caaataaccg gaatcaagaa atatctgggg actacacaat tgaggcttgg 420  
actaagtttg attttccagg gaggggtaat acatactcag actttaaatg gcgttggtat 480  
catttcgatg gtgtagattg ggatcaatca cgacaattcc aaaatcgtat ctacaaattc 540  
cgaggatgat gtaaggcatg ggattgggaa gtagattcgg aaaatggaaa ttatgattat 600  
ttaatgtatg cagatgtaga tatggatcat ccggaggtag taaatgagct tagaagatgg 660  
ggagaatggg atacaaatac attaaatctt gatggattta ggatcgatgc ggtgaagcat 720  
attaaatata gctttacacg tgattgggtg acccatgtaa gaaacgcaac gggaaaagaa 780  
atgtttgctg ttgctgaatt ttggaaaaat gatttaggtg ccttggagaa ctatttaaat 840  
aaaacaaact ggaatcattc tgtctttgat gtcccccttc attataatct ttataacgcg 900  
tcaaatagtg gaggcaacta tgacatggca aaacttctta atggaacggg tgttcaaaag 960  
catccaatgc atgccgtaac ttttgtggat aatcacgatt ctcaacctgg ggaatcatta 1020  
gaatcatttg tacaagaatg gtttaagcca cttgcttatg cgcttatttt aacaagagaa 1080  
caaggctatc cctctgtctt ctatggtgac tactatggaa ttccaacaca tagtgtccca 1140  
gcaatgaaag ccaagattga tccaatctta gaggcgcgtc aaaattttgc atatggaaca 1200  
caacatgatt attttgacca tcataatata atcggatgga cacgtgaagg aaataccacg 1260  
catcccaatt caggacttgc gactatcatg tcggatgggc cagggggaga gaaatggatg 1320  
tacgtagggc aaaataaagc aggtcaagtt tggcatgaca taactggaaa taaaccagga 1380

C1  
CNA

acagttacga tcaatgcaga tggatgggct aatttttcag taaatggagg atctgtttcc 1440  
 atttgggtga aacga 1455

<210> 15  
 <211> 74  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Primer RSERI

<220>  
 <221> misc\_feature  
 <222> (21)..(62)  
 <223> The nucleotides in positions 21-62 were synthesized as: 312234322  
 2 4333313344  
 4233423242 2122112433 43, where 1:(97%A, 1%T, 1%C, 1%G); 2:(97%T,  
 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97%G, 1%A, 1%T,  
 1%C).

<400> 15  
 gcgttttgcc ggccgacata nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60  
 nncaaacctg aatt 74

<210> 16  
 <211> 122  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Primer RSERII

<220>  
 <221> misc\_feature  
 <222> (63)..(104)  
 <223> The nucleotides in positions 73-114 were synthesized as: 31113324  
 1122243113 3414324234 3322333224 2331, where 1:(97%A, 1%T, 1%C,  
 1%G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97  
 %G, 1%A, 1%T, 1%C).

<400> 16  
 gcgttttgcc ggccgacata cattcgcttt gcccaccgg gtccgtctgt tattaatgcc 60  
 gcnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnngccgac aatgtcatgg 120  
 tg 122

<210> 17  
 <211> 78

<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer RSERIII

<220>  
<221> misc\_feature  
<222> (19)..(60)  
<223> The nucleotides in positions 19-60 were synthesized as: 43 341311  
2423 1244244234 1112112312 4324243233, where 1:(97%A, 1%T, 1%C, 1  
%G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97%  
G, 1%A, 1%T, 1%C).

<400> 17  
gtgccttcc cttgtccann nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60  
  
gtacgcatac tgttttct 78

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer FSERIII

<400> 18  
tggacaaggg aaggcgacag 20

<210> 19  
<211> 81  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer RSERV

<220>  
<221> misc\_feature  
<222> (19)..(60)  
<223> The nucleotides in positions 19-60 were synthesized as: 42 422231  
1443 1441122234 3432444142 3233222342, where 1:(97%A, 1%T, 1%C, 1  
%G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97%  
G, 1%A, 1%T, 1%C).

<400> 19  
taagatcggt tcaatttttn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60  
  
cccgtacata tccccgtaga a 81

<210> 20

<211> 18  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer FSERV

<400> 20  
aaaattgaac cgatctta

18

<210> 21  
<211> 107  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer FSERVII

<220>  
<221> misc\_feature  
<222> (54)..(95)  
<223> The nucleotides in positions 54-95 were synthesized as: 3442134 4  
234222331 1431233422 4111234422 13122, where 1:(97%A, 1%T, 1%C, 1  
%G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97%  
G, 1%A, 1%T, 1%C).

<400> 21  
ttccatgctg catcgacaca gggaggcggc tatgatatga ggaaattgct gaannnnnnnn 60  
nnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnntgtcg ataacca 107

<210> 22  
<211> 18  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer RSERVII

<400> 22  
tgtcgatgca gcatggaa

18

<210> 23  
<211> 80  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer FSERIX

<220>  
<221> misc\_feature  
<222> (21)..(62)

C1  
Cm

<223> The nucleotides in positions 21-62 were synthesized as: 432243221  
3 4322221223 2313114441 1232441213 33, where 1:(97%A, 1%T, 1%C, 1  
%G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97%  
G, 1%A, 1%T, 1%C).

<400> 23  
gtccaaacat ggtttaagcc nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60  
nntcagggttt tctacgggga 80

<210> 24  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer RSERIX

<400> 24  
ggcttaaacc atgtttggac 20

<210> 25  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer 1B

<400> 25  
cgattgctga cgctgttatt tgcg 24

<210> 26  
<211> 25  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer #63

<400> 26  
ctatctttga acataaattg aaacc 25

<210> 27  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Forward Primer1

<400> 27

gacctgcagt caggcaacta 20

<210> 28  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Reverse Primer1

<400> 28  
tagagtcgac ctgcaggcat 20

<210> 29  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Forward Primer2

<400> 29  
gacctgcagt caggcaacta 20

<210> 30  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Reverse Primer2

<400> 30  
tagagtcgac ctgcaggcat 20

<210> 31  
<211> 2084  
<212> DNA  
<213> Bacillus amyloliquefaciens

<220>  
<221> misc\_feature  
<222> (343)..(1794)  
<223> CDS

<400> 31  
gccccgcaca tacgaaaaga ctggctgaaa acattgagcc tttgatgact gatgatttgg 60  
ctgaagaagt ggatcgattg tttgagaaaa gaagaagacc ataaaaatac cttgtctgtc 120  
atcagacagg gtatttttta tgctgtccag actgtccgct gtgtaaaaat aaggaataaa 180

C1  
Cont

ggggggttgt tattatthta ctgatatgta aaatataatt tgtataagaa aatgagaggg 240  
 agaggaaaca tgattcaaaa acgaaagcgg acagtthcgt tcagacttgt gcttatgtgc 300  
 acgctgttat ttgtcagtht gccgattaca aaaacatcag cegtaaatgg cacgctgatg 360  
 cagtatthtg aatggtatac gccgaacgac ggccagcatt ggaaacgatt gcagaatgat 420  
 gcggaacatt tatcggatat cggaatcact gccgtctgga thcctccgc atacaaagga 480  
 ttgagccaat ccgataacgg atacggacct tatgatttgt atgatttagg agaattccag 540  
 caaaaaggga cggtcagaac gaaatacggc acaaatcag agcttcaaga tgcgatcggc 600  
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C1  
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